

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Deutsches Krebsforschungszentrum
- (B) STREET: Im Neuenheimer Feld 280
- (C) CITY: Heidelberg
- (E) COUNTRY: Deutschland
- (F) POSTAL CODE (ZIP): 69120

(ii) TITLE OF INVENTION: Protease-related Protein

(iii) NUMBER OF SEQUENCES: 2

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/EP98/05110

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: DE 197 36 198.6
- (B) FILING DATE: 20-AUG-1997

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 61..819

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 61..819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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Sub B11

TAGGTGGTGT CATTCCCCTC CAACCTGAGT GCTGGCAGGT ACACTGCTGG CCACCAGCAG																60
ATG	CCC	ATG	AAG	ATG	CTG	ACA	ATG	AAG	ATG	CTG	GCC	CTG	TGC	TTG	GTT	108
Met	Pro	Met	Lys	Met	Leu	Thr	Met	Lys	Met	Leu	Ala	Leu	Cys	Leu	Val	
1				5				10						15		
CTT	GCT	AAA	TCA	GCC	TGG	TCG	GAG	GAA	CAG	GAG	AAG	GTG	GTT	CAT	GGA	156
Leu	Ala	Lys	Ser	Ala	Trp	Ser	Glu	Glu	Gln	Glu	Lys	Val	Val	His	Gly	
			20					25					30			
GGC	CCG	TGT	TTG	AAG	GAC	TCC	CAC	CCT	TTC	CAG	GCT	GCC	CTC	TAC	ACC	204
Gly	Pro	Cys	Leu	Lys	Asp	Ser	His	Pro	Phe	Gln	Ala	Ala	Leu	Tyr	Thr	
		35					40					45				
TCA	GGT	CAC	TTG	CTG	TGT	GGT	GGG	GTC	CTC	ATT	GAC	CCA	CAG	TGG	GTG	252
Ser	Gly	His	Leu	Leu	Cys	Gly	Gly	Val	Leu	Ile	Asp	Pro	Gln	Trp	Val	
	50					55					60					
CTG	ACA	GCT	GCC	CAC	TGC	AAA	AAA	CCG	AAT	CTG	CAG	GTG	ATC	TTG	GGG	300
Leu	Thr	Ala	Ala	His	Cys	Lys	Lys	Pro	Asn	Leu	Gln	Val	Ile	Leu	Gly	
65					70					75					80	
AAA	CAC	AAC	CTA	CGG	CAA	ACA	GAG	ACT	TTC	CAA	AGG	CAA	ATC	TCA	GTG	348
Lys	His	Asn	Leu	Arg	Gln	Thr	Glu	Thr	Phe	Gln	Arg	Gln	Ile	Ser	Val	
				85					90					95		
GAC	AGG	ACT	ATT	GTC	CAT	CCC	CGC	TAC	AAC	CCT	GAA	ACC	CAC	GAC	AAT	396
Asp	Arg	Thr	Ile	Val	His	Pro	Arg	Tyr	Asn	Pro	Glu	Thr	His	Asp	Asn	
			100					105					110			
GAC	ATC	ATG	ATG	GTG	CAT	CTG	AAA	AAT	CCA	GTC	AAA	TTC	TCT	AAA	AAG	444
Asp	Ile	Met	Met	Val	His	Leu	Lys	Asn	Pro	Val	Lys	Phe	Ser	Lys	Lys	
		115					120					125				
ATC	CAG	CCT	CTG	CCC	TTG	AAG	AAT	GAC	TGC	TCT	GAG	GAG	AAT	CCC	AAC	492
Ile	Gln	Pro	Leu	Pro	Leu	Lys	Asn	Asp	Cys	Ser	Glu	Glu	Asn	Pro	Asn	
	130					135					140					
TGC	CAG	ATC	CTG	GGC	TGG	GGC	AAG	ATG	GAA	AAT	GGT	GAC	TTC	CCA	GAT	540
Cys	Gln	Ile	Leu	Gly	Trp	Gly	Lys	Met	Glu	Asn	Gly	Asp	Phe	Pro	Asp	
145					150					155					160	
ACC	ATT	CAG	TGT	GCT	GAT	GTC	CAT	CTG	GTG	CCC	CGG	GAG	CAG	TGT	GAG	588
Thr	Ile	Gln	Cys	Ala	Asp	Val	His	Leu	Val	Pro	Arg	Glu	Gln	Cys	Glu	
				165					170					175		
CGT	GCC	TAC	CCT	GGC	AAG	ATC	ACC	CAG	AGC	ATG	GTG	TGC	GCA	GGC	GAC	636
Arg	Ala	Tyr	Pro	Gly	Lys	Ile	Thr	Gln	Ser	Met	Val	Cys	Ala	Gly	Asp	
			180					185					190			
ATG	AAA	GAA	GGC	AAC	GAT	TCC	TGT	CAG	GGT	GAT	TCT	GGA	GGT	CCC	CTA	684
Met	Lys	Glu	Gly	Asn	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	
		195					200					205				
GTA	TGT	GGG	GGT	CGC	CTC	CGA	GGG	CTC	GTG	TCA	TGG	GGT	GAC	ATG	CCC	732

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Val	Cys	Gly	Gly	Arg	Leu	Arg	Gly	Leu	Val	Ser	Trp	Gly	Asp	Met	Pro		
210						215					220						
TGT	GGA	TCA	AAG	GAG	AAG	CCA	GGA	GTT	TAC	ACC	GAT	GTC	TGC	ACT	CAT	780	
Cys	Gly	Ser	Lys	Glu	Lys	Pro	Gly	Val	Tyr	Thr	Asp	Val	Cys	Thr	His		
225					230					235					240		
ATC	AGA	TGG	ATC	CAA	AAC	ATC	CTC	AGA	AAC	AAG	TGG	CTG	TGA			822	
Ile	Arg	Trp	Ile	Gln	Asn	Ile	Leu	Arg	Asn	Lys	Trp	Leu					
				245					250								

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Pro	Met	Lys	Met	Leu	Thr	Met	Lys	Met	Leu	Ala	Leu	Cys	Leu	Val		
1				5					10					15			
Leu	Ala	Lys	Ser	Ala	Trp	Ser	Glu	Glu	Gln	Glu	Lys	Val	Val	His	Gly		
			20					25					30				
Gly	Pro	Cys	Leu	Lys	Asp	Ser	His	Pro	Phe	Gln	Ala	Ala	Leu	Tyr	Thr		
		35					40					45					
Ser	Gly	His	Leu	Leu	Cys	Gly	Gly	Val	Leu	Ile	Asp	Pro	Gln	Trp	Val		
	50					55					60						
Leu	Thr	Ala	Ala	His	Cys	Lys	Lys	Pro	Asn	Leu	Gln	Val	Ile	Leu	Gly		
					70					75					80		
Lys	His	Asn	Leu	Arg	Gln	Thr	Glu	Thr	Phe	Gln	Arg	Gln	Ile	Ser	Val		
				85					90					95			
Asp	Arg	Thr	Ile	Val	His	Pro	Arg	Tyr	Asn	Pro	Glu	Thr	His	Asp	Asn		
			100					105					110				
Asp	Ile	Met	Met	Val	His	Leu	Lys	Asn	Pro	Val	Lys	Phe	Ser	Lys	Lys		
		115					120					125					
Ile	Gln	Pro	Leu	Pro	Leu	Lys	Asn	Asp	Cys	Ser	Glu	Glu	Asn	Pro	Asn		
	130					135					140						
Cys	Gln	Ile	Leu	Gly	Trp	Gly	Lys	Met	Glu	Asn	Gly	Asp	Phe	Pro	Asp		
145				150						155					160		
Thr	Ile	Gln	Cys	Ala	Asp	Val	His	Leu	Val	Pro	Arg	Glu	Gln	Cys	Glu		
				165					170					175			

Arg	Ala	Tyr	Pro	Gly	Lys	Ile	Thr	Gln	Ser	Met	Val	Cys	Ala	Gly	Asp
			180					185					190		
Met	Lys	Glu	Gly	Asn	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu
		195					200					205			
Val	Cys	Gly	Gly	Arg	Leu	Arg	Gly	Leu	Val	Ser	Trp	Gly	Asp	Met	Pro
	210					215					220				
Cys	Gly	Ser	Lys	Glu	Lys	Pro	Gly	Val	Tyr	Thr	Asp	Val	Cys	Thr	His
225					230					235					240
Ile	Arg	Trp	Ile	Gln	Asn	Ile	Leu	Arg	Asn	Lys	Trp	Leu			
				245					250						

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